

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2002, 20:03:32 ; Search time 24.96 Seconds
(without alignments)
720.812 Million cell updates/sec

Title: US-09-622-613a-2

Perfect score: 576
Sequence: 1 ODWLTFQKKHLNTRDVDCN.....TFCVTCENQAPVHVGVCNC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.unclassified:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	98.8	127	13	Q918V8
2	395.5	68.7	129	13	Q9DFV6
3	387	67.2	128	13	Q9DFY8
4	317	55.0	128	13	Q9DFY7
5	315	54.7	128	13	Q9DFY5
6	297	51.6	133	13	Q98SM0
7	291	50.5	133	13	Q9PWR7
8	284	49.3	132	13	Q98SM2
9	279	48.4	132	13	Q98SM1
10	277	48.1	133	13	Q98SL9
11	274.5	47.7	132	13	Q9DF78
12	273	47.4	133	13	Q98SL8
13	153.5	26.6	169	13	Q9W738
14	135	23.4	152	11	Q9JK15
15	129	22.4	154	11	Q9JK18
16	128	22.2	157	11	Q9JK19

17	127	22.0	157	11	Q9JKJ3	Q9JKJ3 meriones un
18	126.5	22.0	155	11	Q9JKH9	Q9JKH9 mus pahari
19	126	21.9	157	11	Q9JKJ4	Q9JKJ4 meriones un
20	124	21.5	148	6	Q9GKP9	Q9GKP9 bos taurus
21	123	21.4	157	11	Q9JKJ1	Q9JKJ1 meriones un
22	122.5	21.3	132	6	Q9TV25	Q9TV25 eulemur ful
23	122	21.2	157	11	Q9JKJ2	Q9JKJ2 meriones un
24	121.5	21.1	155	11	Q9JKI4	Q9JKI4 mus saxicol
25	119.5	20.7	170	6	Q9BEC1	Q9BEC1 tragulus ja
26	118.5	20.6	119	6	Q9TV32	Q9TV32 gorilla gor
27	118.5	20.6	153	11	Q9JKI7	Q9JKI7 mus saxicol
28	118	20.5	156	11	Q9JKG6	Q9JKG6 mus caroli
29	117.5	20.4	155	11	Q9RI25	Q9RI25 mus musculu
30	117.5	20.4	155	11	Q9JKG7	Q9JKG7 mus caroli
31	117	20.3	156	11	Q9JKG3	Q9JKG3 mus caroli
32	116.5	20.2	119	6	Q9TS06	Q9TS06 ceropithec
33	116.5	20.2	155	11	Q9JKH8	Q9JKH8 mus pahari
34	116	20.1	156	11	Q9JKH7	Q9JKH7 mus caroli
35	116	20.1	156	11	Q9JKH5	Q9JKH5 mus caroli
36	116	20.1	156	11	Q9JKH4	Q9JKH4 mus caroli
37	116	20.1	156	11	Q9JKG9	Q9JKG9 mus caroli
38	115.5	20.1	155	11	Q9JKI6	Q9JKI6 mus saxicol
39	113	19.6	116	6	Q9TVC0	Q9TVC0 sus scrofa
40	113	19.6	156	11	Q923L6	Q923L6 mus musculu
41	112.5	19.5	132	6	Q9TV24	Q9TV24 galago moho
42	112	19.4	145	6	Q95J16	Q95J16 pan troglod
43	112	19.4	156	11	Q9JKH2	Q9JKH2 mus caroli
44	112	19.4	156	11	Q9JKH1	Q9JKH1 mus caroli
45	111.5	19.4	119	6	Q9TV31	Q9TV31 salimiri scl

ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	127 AA.
Q918V8	Q918V8				
AC	Q918V8:				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	ONCONASE VARIANT RAPLRI PRECURSOR.				
OS	Rana pipiens (Northern leopard frog).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.				
OX	NCBI_TaxId=8404;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER:				
RX	MEDLINE=20330357; PubMed=10871370;				
RA	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.:				
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a				
RT	3' UTR of unusual length and structure."				
RL	Nucleic Acids Res. 28:2375-2382(2000).				
DR	EMBL: AF165133; AAF76935.1; -				
DR	HSSP: P22069; IONC				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: PF00074; fnaseA; 1.				
DR	ProDom: PD000535; RNaseA; 1.				
DR	SMART: SM00092; RNase_Pc; 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.				
KW	Signal.				
FT	SIGNAL	1	23	POTENTIAL.	
SO	SEQUENCE	127 AA;	14491 MW;	B8511DC3407AB69B	CRC64;
Query Match		98.8%;	Score 569;	DB 13;	Length 127;
Best Local Similarity		99.0%;	Pred. No. 1.9e-58;		
Matches	103;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
Oy	1	ODWLTFQKKHLNTRDVDCNIIIMSTNLFHCKDKNTFIYSRPPVKAICGGIATSNVLT	60		
Db	24	ODWLTFQKKHLNTRDVDCNINIMSTNLFHCKDKNTFIYSRPPVKAICGGIATSNVLT	83		

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RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RN Nucleic Acids Res. 28;4097-4104(2000).
RP [2]
RC SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF242553; AAC31439.1; -.
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF000074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL
FT CHAIN 1 23 POTENTIAL.
SO SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match Best Local Similarity 67.2%; Score 387; DB 13; Length 128;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 QDWLFQKKHLTNRDVDCNIMSTNLPHCKDKNTFIYSREPVKAICGIIASKNVLTT 60
Db 24 QNWTFQKKHLTDPRDVDCADMKKALFDCKOKNTFIYARGRVALCALCNITIVSNVLST 83
OY 61 SEFVSDCNVTSRPPCKRYKLKSTNTFCYTGENQAPVHVGVCCHC 104
Db 84 DEFYLSDCNRIRIKLPCHYVKLKSSNTICITCEKRLPVHFVAVEEC 127

RESULT 4
QDFFV7 PRELIMINARY; PRT; 128 AA.
ID QDFFV7 AC QDFFV7
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RC-RNASE3 RIBONUCLEASE PRECURSOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RN Nucleic Acids Res. 28;4097-4104(2000).
DL EMBL; AF242554; AAC31440.2; -.
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF000074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL
FT CHAIN 1 23 POTENTIAL.
SO SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match Best Local Similarity 55.0%; Score 317; DB 13; Length 128;
Matches 57; Conservative 13; Mismatches 34; Indels 0; Gaps 0;

Y 1 QDWLFQKKHLTNRDVDCNIMSTNLPHCKDKNTFIYSREPVKAICGIIASKNVLTT 60
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Db      24 QDMETFOKKHLTDTKKKKCCVEMAKLFDCKKNTFTYALPGRYKALCKNIRONTDLVLSR 83
QY      61 SEFYLSDCNVTSRPKYKLLKSTNTFCVTCENAPVHFVGVGHC 104
Db      84 DAFLLPQCDRIKLPCYKYLKSSSTNTICTTCVNOLPIHFAGVGC 127

RESULT 5
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNASE6 RIBONUCLEASE PRECURSOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Liao Y.-D., Huang H.-C., Liew Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242556; ANG31442.2;
DR HSSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;

Query Match 54.7%; Score 315; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.7e-29;
Matches 56; Conservative 14; Mismatches 34; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLNTRDVCNIIIMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKNLT 60
Db 24 QDMETFOKKHLTDTKKKKCCVEMAKLFDCKKNTFTYALPGRYKALCKNIRONTDLVLSR 83
QY 61 SEFYLSDCNVTSRPKYKLLKSTNTFCVTCENAPVHFVGVGHC 104
Db 84 DAFLLPQCDRIKLPCYKYLKSSSTNTICTTCVNOLPIHFAGVGC 127

RESULT 6
Q98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNASE A-TYPE RIBONUCLEASE RC208 PRECURSOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE-21539506; PubMed-11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351209; AAK30255.1;
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FC122C3499E02 CRC64;

Query Match 51.6%; Score 297; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 7.3e-27;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLNTRDVCNIIIMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKN 56
Db 23 QNMAATFOKKHLNTRDVCNIIIMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKN 81
QY 57 VLTSEFYLSDCNVTSRPKYKLLKSTNTFCVTCENAPVHFVGVGHC 104
Db 82 VLTSTFQKHLNTRDVCNIIIMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKN 132

RESULT 7
Q9PMW7 PRELIMINARY; PRT; 133 AA.
AC Q9PMW7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RIBONUCLEASE PRECURSOR.
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Huang H.-C., Wang S.-C., Liew Y.-J., Lu S.-C., Liao Y.-D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity."
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL: AF039104; AADI0702.1;
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
FT CHAIN 23 133 RIBONUCLEASE.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 50.5%; Score 291; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 3.6e-26;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLNTRDVCNIIIMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKN 56
Db 23 QNMAATFOKKHLNTRDVCNIIIMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKN 81

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OY 57 VLTSEFYISDC--NVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
 DB 82 VLSSTRFOLDICTRTSITPRPCPYSSRTETNYICVGCENQAPVHFGVGHG 132

RESULT 8

O98SM2 8 PRELIMINARY: PRT: 132 AA.

AC O98SM2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNASE A-TYPE RIBONUCLEASE RC203 PRECURSOR.

OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).

DR EMBL; AF351207; AAK30253.1; -.

DR HSSP; P11916; IBC4.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR Prodom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_Pc; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.

KW Signal.

FT SIGNAL.

SO SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 49.3%; Score 284; DB 13; Length 132;
 Best Local Similarity 47.7%; Pred. No. 2.3e-25;

Matches 53; Conservative 14; Mismatches 36; Indels 8; Gaps 3;

OY 1 QDWLTFQKKHLNTRDVCNIIIMSTNLF---HCKDKNTFIYSRPPVKAICGIIASKN 56
 DB 23 QWMAFQCKHPISTSSINNTIMDNNIYIVGQCKKVNFISSATTVVAICNG-VTNSN 81

OY 57 VLTSEFYISDC--NVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
 DB 82 VLSSTRFOLDICTRTSITPRPCPYSSKKTNRKICVGCENQAPVHFGVGHG 132

RESULT 9

O98SM1 9 PRELIMINARY: PRT: 132 AA.

AC O98SM1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNASE A-TYPE RIBONUCLEASE RC204 PRECURSOR.

OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).

DR EMBL; AF351208; AAK30254.1; -.

DR HSSP; P11916; IBC4.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR Prodom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 SO SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 48.4%; Score 279; DB 13; Length 132;
 Best Local Similarity 46.6%; Pred. No. 8.9e-25;

Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

OY 1 QDWLTFQKKHLNTRDVCNIIIMSTNLF---HCKDKNTFIYSRPPVKAICGIIASKN 56
 DB 23 QWMAFQCKHPISTSSINNTIMDNNIYIVGQCKKVNFISSATTVVAICNG-VTNSN 81

OY 57 VLTSEFYISDCN--VTSRPPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
 DB 82 VLSSTRFOLDICTRTSITPRPCPYSSKKTNRKICVGCENQAPVHFGVGHG 132

RESULT 10

O98SL9 10 PRELIMINARY: PRT: 133 AA.

AC O98SL9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNASE A-TYPE RIBONUCLEASE RC212 PRECURSOR.

OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).

DR EMBL; AF351210; AAK30256.1; -.

DR HSSP; P11916; IBC4.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR Prodom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_Pc; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.

KW Signal.

FT SIGNAL.

SO SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 48.1%; Score 277; DB 13; Length 133;
 Best Local Similarity 46.8%; Pred. No. 1.5e-24;

Matches 52; Conservative 17; Mismatches 34; Indels 8; Gaps 3;

OY 1 QDWLTFQKKHLNTRDVCNIIIMSTNLF---HCKDKNTFIYSRPPVKAICGIIASKN 56
 DB 23 QWMAFQCKHPISTSSINNTIMDNNIYIVGQCKKVNFISSATTVVAICNG-VTNSN 81

OY 57 VLTSEFYISDCN--VTSRPPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
 DB 82 VLSSTRFOLDICTRTSITPRPCPYSSRTETNYICVGCENQAPVHFGVGHG 132

RESULT 11

O9DF78 11 PRELIMINARY: PRT: 132 AA.

AC O9DF78;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNASEL1 RIBONUCLEASE PRECURSOR.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF288642; AAG30414.2; -.
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KM Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
FT SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;
SQ

Query Match 47.7%; Score 274.5; DB 13; Length 132;
Best Local Similarity 44.1%; Pred. No. 3e-24;
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;

QY 1 ODWLTFQKKHLNTRDVCNINIMSTNLF---HCKDKNTFIYSRPEPKAICGIIASKN 56
DB 22 QNMATFQKHHTSTSSIDCNTIMDKATIIYVGCKEKERNFTISSDNNKKAICSGVSPDK 81

QY 57 VLTSEFYLSDC---VTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 82 ELSTSFILNLCIRDSITRPPCPVHPSPDNKICVCKEKLQVPHRVGIGKC 132

RESULT 12
098SL8 PRELIMINARY; PRT; 133 AA.
AC 098SL8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNASE A-TYPE RIBONUCLEASE RC218 PRECURSOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.R., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351211; AAK30257.1; -.
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KM Signal.
FT SIGNAL 1 22 POTENTIAL.
FT SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
SQ

Query Match 47.4%; Score 273; DB 13; Length 133;
Best Local Similarity 45.9%; Pred. No. 4.5e-24;
Matches 51; Conservative 18; Mismatches 34; Indels 8; Gaps 3;

QY 1 ODWLTFQKKHLNTRDVCNINIMSTNLF---HCKDKNTFIYSRPEPKAICGIIASKN 56
DB 23 QNMATFQKHHTSTSSIDCNTIMDKATIIYVGCKEKERNFTISSDNNKKAICSGVSPDK 81

QY 57 VLTSEFYLSDC---VTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 82 VLSTKFDLDICTRIFTTRPPCPVHPSPDNKICVCKEKLQVPHRVGIGKC 132

RESULT 13
09W738 PRELIMINARY; PRT; 169 AA.
AC 09W738;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FRU2 PROTEIN.
CN FRU2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7589565;
RA Kinoshita N., Minshall J., Kirschner M.W.;
RT "The identification of two novel ligands of the fgr receptor by a
yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF159166; AAD41901.1; -.
DR HSSP: P00656; 1LSO.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match 26.6%; Score 153.5; DB 13; Length 169;
Best Local Similarity 35.8%; Pred. No. 4.3e-10;
Matches 38; Conservative 20; Mismatches 37; Indels 11; Gaps 6;

QY 6 FQKKHLNTRDVCNINIMSTNLF---HCKDKNTFIYSRPEPKAICGIIASKN 59
DB 33 FMEKHIVGAEETNCNQTIKDRNIRFKNNCKERNFTIHDNCKKYEKAGIYSTFVIS 92

QY 60 TSEFYLSDC---VTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 100
DB 93 KELPLFDLIMGRTPPCVHPSPDNKICVCKEKLQVPHRVGIGKC 138

RESULT 14
09UK15 PRELIMINARY; PRT; 152 AA.
AC 09UK15;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EOSTINOPHIL-ASSOCIATED RIBONUCLEASE 10.
CN EAR10.
OS Mus saxicola (Spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
SQ

